

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/466,343DDATE: 12/10/98
TIME: 14:56:45

INPUT SET: S30278.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: LI, Yi
6
7 (ii) TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
8 CHEMOKINE RECEPTOR HDG NR10 (AS AMENDED)
9
10 (iii) NUMBER OF SEQUENCES: 9
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
14 (B) STREET: 1100 NEW YORK AVE., NW, SUITE 600
15 (C) CITY: WASHINGTON
16 (D) STATE: DC
17 (E) COUNTRY: USA
18 (F) ZIP: 20005
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US 08/466,343
28 (B) FILING DATE: 06-JUN-1995
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: STEFFE, ERIC K.
33 (B) REGISTRATION NUMBER: 36,688
34 (C) REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: (202) 371-2600
38 (B) TELEFAX: (202) 371-2540
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42
43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 1414 base pairs
45 (B) TYPE: nucleic acid
46 (C) STRANDEDNESS: double

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47 (D) TOPOLOGY: linear
48
49 (ii) MOLECULE TYPE: cDNA
50
51
52 (ix) FEATURE:
53 (A) NAME/KEY: CDS
54 (B) LOCATION: 259..1314
55
56
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59 GTGAGATGGT GCTTTCATGA ATTCCCCCAA CAAGAGCCAA GCTCTCCATC TAGTGGACAG 60
60
61 GGAAGCTAGC AGCAAACCTT CCCTTCACTA CGAAACTTCA TTGCTTGGCC CAAAAGAGAG 120
62
63 TTAATTCAAT GTAGACATCT ATGTAGGCAA TTAAAAACCT ATTGATGTAT AAAACAGTTT 180
64
65 GCATTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTATTATTA 240
66
67 TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291
68 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
69 1 5 10
70
71 ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339
72 Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
73 15 20 25
74
75 ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387
76 Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
77 30 35 40
78
79 GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435
80 Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln
81 45 50 55
82
83 AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483
84 Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
85 60 65 70 75
86
87 GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531
88 Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
89 80 85 90
90
91 GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579
92 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu
93 95 100 105
94
95 TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627
96 Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr
97 110 115 120
98
99 ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675

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100	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	
101		125					130					135					
102																	
103	AGG	ACG	GTC	ACC	TTT	GGG	GTG	GTG	ACA	AGT	GTG	ATC	ACT	TGG	GTG	GTG	723
104	Arg	Thr	Val	Thr	Phe	Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Val	Val	
105	140					145					150					155	
106																	
107	GCT	GTG	TTT	GCG	TCT	CTC	CCA	GGA	ATC	ATC	TTT	ACC	AGA	TCT	CAA	AAA	771
108	Ala	Val	Phe	Ala	Ser	Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	
109					160					165						170	
110																	
111	GAA	GGT	CTT	CAT	TAC	ACC	TGC	AGC	TCT	CAT	TTT	CCA	TAC	AGT	CAG	TAT	819
112	Glu	Gly	Leu	His	Tyr	Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	
113				175					180					185			
114																	
115	CAA	TTC	TGG	AAG	AAT	TTC	CAG	ACA	TTA	AAG	ATA	GTC	ATC	TTG	GGG	CTG	867
116	Gln	Phe	Trp	Lys	Asn	Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	Gly	Leu	
117			190					195					200				
118																	
119	GTC	CTG	CCG	CTG	CTT	GTC	ATG	GTC	ATC	TGC	TAC	TCG	GGA	ATC	CTA	AAA	915
120	Val	Leu	Pro	Leu	Leu	Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	
121			205				210						215				
122																	
123	ACT	CTG	CTT	CGG	TGT	CGA	AAT	GAG	AAG	AAG	AGG	CAC	AGG	GCT	GTG	AGG	963
124	Thr	Leu	Leu	Arg	Cys	Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	
125	220					225					230					235	
126																	
127	CTT	ATC	TTC	ACC	ATC	ATG	ATT	GTT	TAT	TTT	CTC	TTC	TGG	GCT	CCC	TAC	1011
128	Leu	Ile	Phe	Thr	Ile	Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	
129					240					245						250	
130																	
131	AAC	ATT	GTC	CTT	CTC	CTG	AAC	ACC	TTC	CAG	GAA	TTC	TTT	GGC	CTG	AAT	1059
132	Asn	Ile	Val	Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Phe	Gly	Leu	Asn	
133				255					260					265			
134																	
135	AAT	TGC	AGT	AGC	TCT	AAC	AGG	TTG	GAC	CAA	GCT	ATG	CAG	GTG	ACA	GAG	1107
136	Asn	Cys	Ser	Ser	Ser	Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	
137			270					275					280				
138																	
139	ACT	CTT	GGG	ATG	ACG	CAC	TGC	TGC	ATC	AAC	CCC	ATC	ATC	TAT	GCC	TTT	1155
140	Thr	Leu	Gly	Met	Thr	His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	
141			285				290					295					
142																	
143	GTC	GGG	GAG	AAG	TTC	AGA	AAC	TAC	CTC	TTA	GTC	TTC	TTC	CAA	AAG	CAC	1203
144	Val	Gly	Glu	Lys	Phe	Arg	Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	His	
145	300					305					310					315	
146																	
147	ATT	GCC	AAA	CGC	TTC	TGC	AAA	TGC	TGT	TCT	ATT	TTC	CAG	CAA	GAG	GCT	1251
148	Ile	Ala	Lys	Arg	Phe	Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu	Ala	
149					320					325						330	
150																	
151	CCC	GAG	CGA	GCA	AGC	TCA	GTT	TAC	ACC	CGA	TCC	ACT	GGG	GAG	CAG	GAA	1299
152	Pro	Glu	Arg	Ala	Ser	Ser	Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu	Gln	Glu	

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153          335          340          345
154
155 ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG      1354
156 Ile Ser Val Gly Leu
157      350
158
159 TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCTTTT      1414
160
161
162
163 (2) INFORMATION FOR SEQ ID NO:2:
164
165     (i) SEQUENCE CHARACTERISTICS:
166         (A) LENGTH: 352 amino acids
167         (B) TYPE: amino acid
168         (D) TOPOLOGY: linear
169
170     (ii) MOLECULE TYPE: protein
171
172     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
173
174 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
175   1          5          10          15
176
177 Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
178      20          25          30
179
180 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
181      35          40          45
182
183 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg Leu Glu Ser Met
184      50          55          60
185
186 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
187      65          70          75          80
188
189 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
190      85          90          95
191
192 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
193      100         105         110
194
195 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
196      115         120         125
197
198 Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
199      130         135         140
200
201 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
202      145         150         155         160
203
204 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
205      165         170         175

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206
207 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
208           180           185           190
209
210 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
211           195           200           205
212
213 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
214           210           215           220
215
216 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
217 225           230           235           240
218
219 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
220           245           250           255
221
222 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
223           260           265           270
224
225 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
226           275           280           285
227
228 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
229           290           295           300
230
231 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
232 305           310           315           320
233
234 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
235           325           330           335
236
237 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
238           340           345           350
239

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCCT CCATGGATTA TCAAGTGTCA

30

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 BASE PAIRS

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text